



SEQUENCE LISTING

<110> Osteryoung, Katherine W.

<120> Manipulation of Min Genes in Plants

<130> 920905.90041

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<150> 60/130,403

<151> 1999-04-19

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<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> *Arabidopsis thaliana*

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<221> CDS

<222> (1)..(978)

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cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc	96
Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val	
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aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat	144
Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn	
35 40 45	
cgc aaa ccg gaa ctc gcc gga aac acg ccg cgt atc gtc gtt atc acc	192
Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr	
50 55 60	
tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt	240
Ser Gly Lys Gly Val Gly Lys Thr Thr Thr Ala Asn Val Gly	
65 70 75 80	
ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac	288
Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp	
85 90 95	
ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc	336
Leu Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu Asn Arg Val	
100 105 110	
aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa	384
Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln	
115 120 125	

gct ctg gta cgt gat aag cgt tgg tcg aat ttc gaa ttg cta tgt ata Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile 130 135 140	432
tct aaa cct aga tcg aaa ctt ccg atg gga ttt ggt aaa gca ttg Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu 145 150 155 160	480
gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp 165 170 175	528
ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr 180 185 190	576
gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile 195 200 205	624
aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp 210 215 220	672
gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met 225 230 235 240	720
att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu 245 250 255	768
gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg 260 265 270	816
agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct cct acg ctt Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu 275 280 285	864
gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp 290 295 300	912
agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc Ser Met Lys Ala Val Met Val Glu Glu Pro Lys Lys Arg Gly Phe 305 310 315 320	960
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 35 40 45
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 65 70 75 80
 Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp
 85 90 95
 Leu Gly Leu Arg Asn Leu Asp Leu Leu Gly Leu Glu Asn Arg Val
 100 105 110
 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln
 115 120 125
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 130 135 140
 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu
 145 150 155 160
 Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp
 165 170 175
 Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr
 180 185 190
 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile
 195 200 205
 Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp
 210 215 220
 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met
 225 230 235 240
 Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu
 245 250 255
 Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg
 260 265 270
 Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu
 275 280 285
 Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp
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 Phe Ser Phe Phe Gly Gly
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Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser Thr Phe Pro
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aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc 154
Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr Pro Lys Pro
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tac cca aag cca cca att cgc tcc gtc ctt caa tac aat cgc aaa 202
Tyr Pro Lys Pro Pro Ile Arg Ser Val Leu Gln Tyr Asn Arg Lys
40 45 50

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Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile Asp Ala Asp
55 60 65

gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa aac cgc gtc 298
Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val
70 75 80

aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa 346
Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln
85 90 95

gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att 394
Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile
100 105 110 115

tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta 442
Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu
120 125 130

gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc ccg gat ttt 490
Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe
135 140 145

ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc 538
Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala
150 155 160

att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act 586
Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr
165 170 175

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 100 105 110
 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
 115 120 125
 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
 130 135 140
 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
 145 150 155 160
 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
 165 170 175
 Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
 180 185 190
 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
 195 200 205
 Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
 210 215 220
 Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
 225 230 235 240
 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
 245 250 255
 Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
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• <210> 6
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• <212> DNA
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